

## SEQUENCE LISTING

- <110> BASF Aktiengesellschaft
- 5 <120> Electron donor system for enzymes and its use in the biochemical conversion of substrates
- <130> M/40076
- 10 <140>  
<141>
- <160> 35
- 15 <170> PatentIn Ver. 2.1
- <210> 1  
<211> 36  
<212> DNA  
<213> Artificial sequence
- 20 <220>  
<223> Description of the artificial sequence:  
Oligonucleotide for genomic Bacillus  
megaterium DNA
- 25 <400> 1  
gtgaaagagg gatcccatga caattaaaga aatgcc 36
- <210> 2
- 30 <211> 38  
<212> DNA  
<213> Artificial sequence
- <220>  
<223> Description of the artificial sequence:  
Oligonucleotide for genomic Bacillus  
megaterium DNA
- 35 <400> 2  
gcctcttgga tccttaccca gccacacgt cttttgcg 38
- 40 <210> 3  
<211> 19  
<212> DNA  
<213> Artificial sequence
- 45 <220>

10031241.011702

## 56

<223> Description of the artificial sequence: Primer for sequencing

<400> 3

5 gtacgtgatt ttgcaggag

19

<210> 4

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<212> DNA

10 <213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer for sequencing

15

<400> 4

ggctatcatg cgatgatggt

20

<210> 5

20 <211> 19

<212> DNA

<213> Artificial sequence

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25 <223> Description of the artificial sequence: Primer for sequencing

<400> 5

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30

<210> 6

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<212> DNA

<213> Artificial sequence

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<220>

<223> Description of the artificial sequence: Primer for sequencing

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40 ggaaaagatc cagaaacggg

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<210> 7

<211> 19

45 <212> DNA

<213> Artificial sequence

<220>

0031241.011702

## 57

<223> Description of the artificial sequence: Primer for sequencing

<400> 7

5 gtcggcatgg tcttaaacg

19

<210> 8

<211> 20

<212> DNA

10 <213> Artificial sequence

<220>

<223> Description of the artificial sequence: Primer for sequencing

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attcctcagc ttcaccgtga

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<210> 9

20 <211> 19

<212> DNA

<213> Artificial sequence

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25 <223> Description of the artificial sequence: Primer for sequencing

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cttggcggta ttccttcac

19

30

<210> 10

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<212> DNA

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<223> Description of the artificial sequence: Primer for sequencing

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atttgaccg caggtcgcaa

20

40

<210> 11

<211> 17

<212> DNA

45 <213> Artificial sequence

<220>

20251101 10:44:41

## 58

<223> Description of the artificial sequence: Primer for sequencing

<400> 11  
5 ctgggctact acgtatc 17

<210> 12  
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<212> DNA  
10 <213> Artificial sequence

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<223> Description of the artificial sequence: Primer for sequencing

15 <400> 12  
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<210> 13  
20 <211> 19  
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<210> 15  
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<220>

0001241.01102

## 59

<223> Description of the artificial sequence: Primer for sequencing

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5 cgatttcttc atcacctc

18

<210> 16

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<212> DNA

10 <213> Artificial sequence

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<223> Description of the artificial sequence: Primer for sequencing

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20

<210> 17

20 <211> 20

<212> DNA

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25 <223> Description of the artificial sequence: Primer for sequencing

<400> 17

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30 <210> 18

<211> 20

<212> DNA

<213> Artificial sequence

35 <220>

<223> Description of the artificial sequence: Primer for sequencing

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20

<210> 19

<211> 20

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45 <213> Artificial sequence

10031244.011700

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&lt;223&gt; Description of the artificial sequence: Primer for sequencing

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20

&lt;210&gt; 20

&lt;211&gt; 20

10 &lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of the artificial sequence: Primer for sequencing

15

&lt;400&gt; 20

ttgcgacctg cggtgcaaatt

20

20 &lt;210&gt; 21

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

25 &lt;220&gt;

&lt;223&gt; Description of the artificial sequence: Primer for sequencing

&lt;400&gt; 21

ggcgctgtcg acaaattgaa

20

30

&lt;210&gt; 22

&lt;211&gt; 20

&lt;212&gt; DNA

35 &lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Description of the artificial sequence: Primer for sequencing

40 &lt;400&gt; 22

ttttagcagc cattgcgcca

20

&lt;210&gt; 23

45 &lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

10031344.011703

&lt;220&gt;

&lt;223&gt; Description of the artificial sequence: Primer for sequencing

5 &lt;400&gt; 23

gtttcagggt cttttggcag

20

&lt;210&gt; 24

&lt;211&gt; 36

10 &lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

15 <223> Description of the artificial sequence:  
Oligonucleotide for tag at C terminus

&lt;400&gt; 24

gtgaaagagg gatcccatga caattaaaga aatgcc

36

20 &lt;210&gt; 25

&lt;211&gt; 42

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

25 &lt;220&gt;

<223> Description of the artificial sequence:  
Oligonucleotide for tag at C terminus

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30 cggaattctt aacgacgacg acgacgacgc ccagcccaca cg

42

&lt;210&gt; 26

&lt;211&gt; 36

&lt;212&gt; DNA

35 &lt;213&gt; Artificial sequence

&lt;220&gt;

<223> Description of the artificial sequence:  
Oligonucleotide for tag at C terminus

40 &lt;400&gt; 26

gtgaaagagg gatcccatga caattaaaga aatgcc

36

&lt;210&gt; 27

45 &lt;211&gt; 42

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

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<220>

<223> Description of the artificial sequence:  
Oligonucleotide for tag at C terminus

5 <400> 27

cggaattctt attcttcttc ttcttcttcc ccagcccaca cg

42

<210> 28

<211> 36

10 <212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence:  
Oligonucleotide for tag at C terminus

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<400> 28

gtgaaagagg gatcccatga caattaaaga aatgcc

36

20 <210> 29

<211> 42

<212> DNA

<213> Artificial sequence

25 <220>

<223> Description of the artificial sequence:  
Oligonucleotide for tag at C terminus

<400> 29

cgcaattctt aatgatgatg atgatgatgc ccagcccaca cg

42

30

<210> 30

<211> 38

<212> DNA

35 <213> Artificial sequence

<220>

<223> Description of the artificial sequence:  
Oligonucleotide for tag at C terminus

40 <400> 30

gtctcagcgt gagaccccca gccacacgt cttttgcc

38

<210> 31

<211> 36

45 <212> DNA

<213> Artificial sequence

0031241.011709



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<223> Description of the artificial sequence:  
Oligonucleotide for tag at C terminus

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gtgaaagagg tctccaatga caattaaaga aatgcc

36

&lt;210&gt; 32

&lt;211&gt; 34

10 &lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

15 <223> Description of the artificial sequence: Primer for  
P450 BM-3 point mutant F87A

&lt;400&gt; 32

gcaggagacg ggttgccac aagctggacg catg

34

20 &lt;210&gt; 33

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

25 &lt;220&gt;

<223> Description of the artificial sequence: Primer for  
P450 BM-3 point mutant F87A

&lt;400&gt; 33

catgcgtcca gcttgtggcc aaccgctctc ctgc

34

30

&lt;210&gt; 34

&lt;211&gt; 3150

&lt;212&gt; DNA

&lt;213&gt; Bacillus megaterium

35

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (4)..(3150)

&lt;400&gt; 34

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Thr Ile Lys Glu Met Pro Gln Pro Lys Thr Phe Gly Glu Leu Lys

1

5

10

15

aat tta ccg tta tta aac aca gat aaa ccg gtt caa gct ttg atg aaa 96

45 Asn Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys

20

25

30

att gcg gat gaa tta gga gaa atc ttt aaa ttc gag gcg cct ggt cgt 144

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64

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	gta	acg	cgc	tac	tta	tca	agt	cag	cgt	cta	att	aaa	gaa	gca	tgc	gat	192
5	Val	Thr	Arg	Tyr	Leu	Ser	Ser	Gln	Arg	Leu	Ile	Lys	Glu	Ala	Cys	Asp	
			50					55					60				
	gaa	tca	cgc	ttt	gat	aaa	aac	tta	agt	caa	gcg	ctt	aaa	ttt	gta	cgt	240
	Glu	Ser	Arg	Phe	Asp	Lys	Asn	Leu	Ser	Gln	Ala	Leu	Lys	Phe	Val	Arg	
			65				70					75					
10	gat	ttt	gca	gga	gac	ggg	tta	ttt	aca	agc	tgg	acg	cat	gaa	aaa	aat	288
	Asp	Phe	Ala	Gly	Asp	Gly	Leu	Phe	Thr	Ser	Trp	Thr	His	Glu	Lys	Asn	
			80				85				90					95	
	tgg	aaa	aaa	gcg	cat	aat	atc	tta	ctt	cca	agc	ttc	agt	cag	cag	gca	336
15	Trp	Lys	Lys	Ala	His	Asn	Ile	Leu	Leu	Pro	Ser	Phe	Ser	Gln	Gln	Ala	
					100					105					110		
	atg	aaa	ggc	tat	cat	gcg	atg	atg	gtc	gat	atc	gcc	gtg	cag	ctt	gtt	384
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20				115					120					125			
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	tat	cgc	ttt	aac	agc	ttt	tac	cga	gat	cag	cct	cat	cca	ttt	att	aca	528
30	Tyr	Arg	Phe	Asn	Ser	Phe	Tyr	Arg	Asp	Gln	Pro	His	Pro	Phe	Ile	Thr	
			160			165				170					175		
	agt	atg	gtc	cgt	gca	ctg	gat	gaa	gca	atg	aac	aag	ctg	cag	cga	gca	576
	Ser	Met	Val	Arg	Ala	Leu	Asp	Glu	Ala	Met	Asn	Lys	Leu	Gln	Arg	Ala	
35				180					185					190			
	aat	cca	gac	gac	cca	gct	tat	gat	gaa	aac	aag	cgc	cag	ttt	caa	gaa	624
	Asn	Pro	Asp	Asp	Pro	Ala	Tyr	Asp	Glu	Asn	Lys	Arg	Gln	Phe	Gln	Glu	
			195					200					205				
40	gat	atc	aag	gtg	atg	aac	gac	cta	gta	gat	aaa	att	att	gca	gat	cgc	672
	Asp	Ile	Lys	Val	Met	Asn	Asp	Leu	Val	Asp	Lys	Ile	Ile	Ala	Asp	Arg	
			210				215					220					
	aaa	gca	agc	ggg	gaa	caa	agc	gat	gat	tta	tta	acg	cat	atg	cta	aac	720
45	Lys	Ala	Ser	Gly	Glu	Gln	Ser	Asp	Asp	Leu	Leu	Thr	His	Met	Leu	Asn	
			225				230					235					
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## 65

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5	Tyr	Gln	Ile	Ile	Thr	Phe	Leu	Ile	Ala	Gly	His	Glu	Thr	Thr	Ser	Gly	
					260					265					270		
	ctt	tta	tca	ttt	gcg	ctg	tat	ttc	tta	gtg	aaa	aat	cca	cat	gta	tta	864
	Leu	Leu	Ser	Phe	Ala	Leu	Tyr	Phe	Leu	Val	Lys	Asn	Pro	His	Val	Leu	
				275					280					285			
10	caa	aaa	gca	gca	gaa	gaa	gca	gca	cga	gtt	cta	gta	gat	cct	gtt	cca	912
	Gln	Lys	Ala	Ala	Glu	Glu	Ala	Ala	Arg	Val	Leu	Val	Asp	Pro	Val	Pro	
			290					295					300				
15	agc	tac	aaa	caa	gtc	aaa	cag	ctt	aaa	tat	gtc	ggc	atg	gtc	tta	aac	960
	Ser	Tyr	Lys	Gln	Val	Lys	Gln	Leu	Lys	Tyr	Val	Gly	Met	Val	Leu	Asn	
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20	Glu	Ala	Leu	Arg	Leu	Trp	Pro	Thr	Ala	Pro	Ala	Phe	Ser	Leu	Tyr	Ala	
	320					325					330					335	
	aaa	gaa	gat	acg	gtg	ctt	gga	gga	gaa	tat	cct	tta	gaa	aaa	ggc	gac	1056
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				340						345					350		
25	gaa	cta	atg	gtt	ctg	att	cct	cag	ctt	cac	cgt	gat	aaa	aca	att	tgg	1104
	Glu	Leu	Met	Val	Leu	Ile	Pro	Gln	Leu	His	Arg	Asp	Lys	Thr	Ile	Trp	
				355					360					365			
	gga	gac	gat	gtg	gaa	gag	ttc	cgt	cca	gag	cgt	ttt	gaa	aat	cca	agt	1152
30	Gly	Asp	Asp	Val	Glu	Glu	Phe	Arg	Pro	Glu	Arg	Phe	Glu	Asn	Pro	Ser	
		370						375					380				
	gcg	att	ccg	cag	cat	gcg	ttt	aaa	ccg	ttt	gga	aac	ggt	cag	cgt	gcg	1200
35	Ala	Ile	Pro	Gln	His	Ala	Phe	Lys	Pro	Phe	Gly	Asn	Gly	Gln	Arg	Ala	
		385						390				395					
	tgt	atc	ggt	cag	cag	ttc	gct	ctt	cat	gaa	gca	acg	ctg	gta	ctt	ggt	1248
	Cys	Ile	Gly	Gln	Gln	Phe	Ala	Leu	His	Glu	Ala	Thr	Leu	Val	Leu	Gly	
	400					405					410					415	
40	atg	atg	cta	aaa	cac	ttt	gac	ttt	gaa	gat	cat	aca	aac	tac	gag	ctg	1296
	Met	Met	Leu	Lys	His	Phe	Asp	Phe	Glu	Asp	His	Thr	Asn	Tyr	Glu	Leu	
					420					425					430		
	gat	att	aaa	gaa	act	tta	acg	tta	aaa	cct	gaa	ggc	ttt	gtg	gta	aaa	1344
45	Asp	Ile	Lys	Glu	Thr	Leu	Thr	Leu	Lys	Pro	Glu	Gly	Phe	Val	Val	Lys	
				435					440					445			
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## 66

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	gaa	cag	tct	gct	aaa	aaa	gta	cgc	aaa	aag	gca	gaa	aac	gct	cat	aat	1440
5	Glu	Gln	Ser	Ala	Lys	Lys	Val	Arg	Lys	Lys	Ala	Glu	Asn	Ala	His	Asn	
	465						470					475					
	acg	ccg	ctg	ctt	gtg	cta	tac	ggt	tca	aat	atg	gga	aca	gct	gaa	gga	1488
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10	acg	gcg	cgt	gat	tta	gca	gat	att	gca	atg	agc	aaa	gga	ttt	gca	ccg	1536
	Thr	Ala	Arg	Asp	Leu	Ala	Asp	Ile	Ala	Met	Ser	Lys	Gly	Phe	Ala	Pro	
	500									505					510		
15	cag	gtc	gca	acg	ctt	gat	tca	cac	gcc	gga	aat	ctt	ccg	cgc	gaa	gga	1584
	Gln	Val	Ala	Thr	Leu	Asp	Ser	His	Ala	Gly	Asn	Leu	Pro	Arg	Glu	Gly	
	515								520					525			
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	Asp	Phe	Glu	Gly	Thr	Tyr	Glu	Glu	Trp	Arg	Glu	His	Met	Trp	Ser	Asp	
	610							615					620				
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	Val	Ala	Ala	Tyr	Phe	Asn	Leu	Asp	Ile	Glu	Asn	Ser	Glu	Asp	Asn	Lys	
	625						630					635					
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45	Ser	Thr	Leu	Ser	Leu	Gln	Phe	Val	Asp	Ser	Ala	Ala	Asp	Met	Pro	Leu	
	640					645					650				655		
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## 67

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5	Leu	Gln	Gln	Pro	Gly	Ser	Ala	Arg	Ser	Thr	Arg	His	Leu	Glu	Ile	Glu	
				675					680					685			
	ctt	cca	aaa	gaa	gct	tct	tat	caa	gaa	gga	gat	cat	tta	ggg	gtt	att	2112
	Leu	Pro	Lys	Glu	Ala	Ser	Tyr	Gln	Glu	Gly	Asp	His	Leu	Gly	Val	Ile	
				690				695					700				
10	cct	cgc	aac	tat	gaa	gga	ata	gta	aac	cgt	gta	aca	gca	agg	ttc	ggc	2160
	Pro	Arg	Asn	Tyr	Glu	Gly	Ile	Val	Asn	Arg	Val	Thr	Ala	Arg	Phe	Gly	
				705			710					715					
	cta	gat	gca	tca	cag	caa	atc	cgt	ctg	gaa	gca	gaa	gaa	gaa	aaa	tta	2208
15	Leu	Asp	Ala	Ser	Gln	Gln	Ile	Arg	Leu	Glu	Ala	Glu	Glu	Glu	Lys	Leu	
	720				725					730					735		
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	Ala	His	Leu	Pro	Leu	Ala	Lys	Thr	Val	Ser	Val	Glu	Glu	Leu	Leu	Gln	
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	Tyr	Val	Glu	Leu	Gln	Asp	Pro	Val	Thr	Arg	Thr	Gln	Leu	Arg	Ala	Met	
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25	Ala	Ala	Lys	Thr	Val	Cys	Pro	Pro	His	Lys	Val	Glu	Leu	Glu	Ala	Leu	
			770				775					780					
	ctt	gaa	aag	caa	gcc	tac	aaa	gaa	caa	gtg	ctg	gca	aaa	cgt	tta	aca	2400
30	Leu	Glu	Lys	Gln	Ala	Tyr	Lys	Glu	Gln	Val	Leu	Ala	Lys	Arg	Leu	Thr	
		785					790					795					
	atg	ctt	gaa	ctg	ctt	gaa	aaa	tac	ccg	gcg	tgt	gaa	atg	aaa	ttc	agc	2448
	Met	Leu	Glu	Leu	Leu	Glu	Lys	Tyr	Pro	Ala	Cys	Glu	Met	Lys	Phe	Ser	
35	800					805				810					815		
	gaa	ttt	atc	gcc	ctt	ctg	cca	agc	ata	cgc	ccg	cgc	tat	tac	tcg	att	2496
	Glu	Phe	Ile	Ala	Leu	Leu	Pro	Ser	Ile	Arg	Pro	Arg	Tyr	Tyr	Ser	Ile	
				820					825				830				
	tct	tca	tca	cct	cgt	gtc	gat	gaa	aaa	caa	gca	agc	atc	acg	gtc	agc	2544
40	Ser	Ser	Ser	Pro	Arg	Val	Asp	Glu	Lys	Gln	Ala	Ser	Ile	Thr	Val	Ser	
				835				840					845				
	gtt	gtc	tca	gga	gaa	gcg	tgg	agc	gga	tat	gga	gaa	tat	aaa	gga	att	2592
45	Val	Val	Ser	Gly	Glu	Ala	Trp	Ser	Gly	Tyr	Gly	Glu	Tyr	Lys	Gly	Ile	
			850				855					860					
	gcg	tcg	aac	tat	ctt	gcc	gag	ctg	caa	gaa	gga	gat	acg	att	acg	tgc	2640

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## 68

	Ala	Ser	Asn	Tyr	Leu	Ala	Glu	Leu	Gln	Glu	Gly	Asp	Thr	Ile	Thr	Cys	
	865						870					875					
	ttt	att	tcc	aca	ccg	cag	tca	gaa	ttt	acg	ctg	cca	aaa	gac	cct	gaa	2688
5	Phe	Ile	Ser	Thr	Pro	Gln	Ser	Glu	Phe	Thr	Leu	Pro	Lys	Asp	Pro	Glu	
	880					885					890					895	
	acg	ccg	ctt	atc	atg	gtc	gga	ccg	gga	aca	ggc	gtc	gcg	ccg	ttt	aga	2736
	Thr	Pro	Leu	Ile	Met	Val	Gly	Pro	Gly	Thr	Gly	Val	Ala	Pro	Phe	Arg	
					900					905					910		
10	ggc	ttt	gtg	cag	gcg	cgc	aaa	cag	cta	aaa	gaa	caa	gga	cag	tca	ctt	2784
	Gly	Phe	Val	Gln	Ala	Arg	Lys	Gln	Leu	Lys	Glu	Gln	Gly	Gln	Ser	Leu	
				915					920					925			
	gga	gaa	gca	cat	tta	tac	ttc	ggc	tgc	cgt	tca	cct	cat	gaa	gac	tat	2832
15	Gly	Glu	Ala	His	Leu	Tyr	Phe	Gly	Cys	Arg	Ser	Pro	His	Glu	Asp	Tyr	
			930					935					940				
	ctg	tat	caa	gaa	gag	ctt	gaa	aac	gcc	caa	agc	gaa	ggc	atc	att	acg	2880
20	Leu	Tyr	Gln	Glu	Glu	Leu	Glu	Asn	Ala	Gln	Ser	Glu	Gly	Ile	Ile	Thr	
		945					950					955					
	ctt	cat	acc	gct	ttt	tct	cgc	atg	cca	aat	cag	ccg	aaa	aca	tac	gtt	2928
	Leu	His	Thr	Ala	Phe	Ser	Arg	Met	Pro	Asn	Gln	Pro	Lys	Thr	Tyr	Val	
		960				965					970				975		
25	cag	cac	gta	atg	gaa	caa	gac	ggc	aag	aaa	ttg	att	gaa	ctt	ctt	gat	2976
	Gln	His	Val	Met	Glu	Gln	Asp	Gly	Lys	Lys	Leu	Ile	Glu	Leu	Leu	Asp	
				980					985					990			
	caa	gga	gcg	cac	ttc	tat	att	tgc	gga	gac	gga	agc	caa	atg	gca	cct	3024
30	Gln	Gly	Ala	His	Phe	Tyr	Ile	Cys	Gly	Asp	Gly	Ser	Gln	Met	Ala	Pro	
			995					1000					1005				
	gcc	gtt	gaa	gca	acg	ctt	atg	aaa	agc	tat	gct	gac	gtt	cac	caa	gtg	3072
	Ala	Val	Glu	Ala	Thr	Leu	Met	Lys	Ser	Tyr	Ala	Asp	Val	His	Gln	Val	
35			1010					1015					1020				
	agt	gaa	gca	gac	gct	cgc	tta	tgg	ctg	cag	cag	cta	gaa	gaa	aaa	ggc	3120
	Ser	Glu	Ala	Asp	Ala	Arg	Leu	Trp	Leu	Gln	Gln	Leu	Glu	Glu	Lys	Gly	
		1025				1030						1035					
40	cga	tac	gca	aaa	gac	gtg	tgg	gct	ggg	taa							3150
	Arg	Tyr	Ala	Lys	Asp	Val	Trp	Ala	Gly								
		1040				1045											
45	<210>	35															
	<211>	1048															
	<212>	PRT															
	<213>	Bacillus megaterium															

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&lt;400&gt; 35

Thr Ile Lys Glu Met Pro Gln Pro Lys Thr Phe Gly Glu Leu Lys Asn  
 1 5 10 15  
 5 Leu Pro Leu Leu Asn Thr Asp Lys Pro Val Gln Ala Leu Met Lys Ile  
 20 25 30  
 Ala Asp Glu Leu Gly Glu Ile Phe Lys Phe Glu Ala Pro Gly Arg Val  
 35 40 45  
 10 Thr Arg Tyr Leu Ser Ser Gln Arg Leu Ile Lys Glu Ala Cys Asp Glu  
 50 55 60  
 Ser Arg Phe Asp Lys Asn Leu Ser Gln Ala Leu Lys Phe Val Arg Asp  
 15 65 70 75 80  
 Phe Ala Gly Asp Gly Leu Phe Thr Ser Trp Thr His Glu Lys Asn Trp  
 85 90 95  
 Lys Lys Ala His Asn Ile Leu Leu Pro Ser Phe Ser Gln Gln Ala Met  
 20 100 105 110  
 Lys Gly Tyr His Ala Met Met Val Asp Ile Ala Val Gln Leu Val Gln  
 115 120 125  
 25 Lys Trp Glu Arg Leu Asn Ala Asp Glu His Ile Glu Val Pro Glu Asp  
 130 135 140  
 Met Thr Arg Leu Thr Leu Asp Thr Ile Gly Leu Cys Gly Phe Asn Tyr  
 145 150 155 160  
 30 Arg Phe Asn Ser Phe Tyr Arg Asp Gln Pro His Pro Phe Ile Thr Ser  
 165 170 175  
 Met Val Arg Ala Leu Asp Glu Ala Met Asn Lys Leu Gln Arg Ala Asn  
 180 185 190  
 35 Pro Asp Asp Pro Ala Tyr Asp Glu Asn Lys Arg Gln Phe Gln Glu Asp  
 195 200 205  
 Ile Lys Val Met Asn Asp Leu Val Asp Lys Ile Ile Ala Asp Arg Lys  
 210 215 220  
 40 Ala Ser Gly Glu Gln Ser Asp Asp Leu Leu Thr His Met Leu Asn Gly  
 225 230 235 240  
 Lys Asp Pro Glu Thr Gly Glu Pro Leu Asp Asp Glu Asn Ile Arg Tyr  
 245 250 255  
 45 Gln Ile Ile Thr Phe Leu Ile Ala Gly His Glu Thr Thr Ser Gly Leu  
 260 265 270

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Leu Ser Phe Ala Leu Tyr Phe Leu Val Lys Asn Pro His Val Leu Gln  
 275 280 285

5 Lys Ala Ala Glu Glu Ala Ala Arg Val Leu Val Asp Pro Val Pro Ser  
 290 295 300

Tyr Lys Gln Val Lys Gln Leu Lys Tyr Val Gly Met Val Leu Asn Glu  
 305 310 315 320

10 Ala Leu Arg Leu Trp Pro Thr Ala Pro Ala Phe Ser Leu Tyr Ala Lys  
 325 330 335

Glu Asp Thr Val Leu Gly Gly Glu Tyr Pro Leu Glu Lys Gly Asp Glu  
 340 345 350

15 Leu Met Val Leu Ile Pro Gln Leu His Arg Asp Lys Thr Ile Trp Gly  
 355 360 365

Asp Asp Val Glu Glu Phe Arg Pro Glu Arg Phe Glu Asn Pro Ser Ala  
 370 375 380

20 Ile Pro Gln His Ala Phe Lys Pro Phe Gly Asn Gly Gln Arg Ala Cys  
 385 390 395 400

Ile Gly Gln Gln Phe Ala Leu His Glu Ala Thr Leu Val Leu Gly Met  
 405 410 415

25 Met Leu Lys His Phe Asp Phe Glu Asp His Thr Asn Tyr Glu Leu Asp  
 420 425 430

Ile Lys Glu Thr Leu Thr Leu Lys Pro Glu Gly Phe Val Val Lys Ala  
 435 440 445

Lys Ser Lys Lys Ile Pro Leu Gly Gly Ile Pro Ser Pro Ser Thr Glu  
 450 455 460

35 Gln Ser Ala Lys Lys Val Arg Lys Lys Ala Glu Asn Ala His Asn Thr  
 465 470 475 480

Pro Leu Leu Val Leu Tyr Gly Ser Asn Met Gly Thr Ala Glu Gly Thr  
 485 490 495

40 Ala Arg Asp Leu Ala Asp Ile Ala Met Ser Lys Gly Phe Ala Pro Gln  
 500 505 510

Val Ala Thr Leu Asp Ser His Ala Gly Asn Leu Pro Arg Glu Gly Ala  
 515 520 525

45 Val Leu Ile Val Thr Ala Ser Tyr Asn Gly His Pro Pro Asp Asn Ala  
 530 535 540

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## 71

Lys Gln Phe Val Asp Trp Leu Asp Gln Ala Ser Ala Asp Glu Val Lys  
 545 550 555 560  
 Gly Val Arg Tyr Ser Val Phe Gly Cys Gly Asp Lys Asn Trp Ala Thr  
 565 570 575  
 5 Thr Tyr Gln Lys Val Pro Ala Phe Ile Asp Glu Thr Leu Ala Ala Lys  
 580 585 590  
 Gly Ala Glu Asn Ile Ala Asp Arg Gly Glu Ala Asp Ala Ser Asp Asp  
 10 595 600 605  
 Phe Glu Gly Thr Tyr Glu Glu Trp Arg Glu His Met Trp Ser Asp Val  
 610 615 620  
 15 Ala Ala Tyr Phe Asn Leu Asp Ile Glu Asn Ser Glu Asp Asn Lys Ser  
 625 630 635 640  
 Thr Leu Ser Leu Gln Phe Val Asp Ser Ala Ala Asp Met Pro Leu Ala  
 645 650 655  
 20 Lys Met His Gly Ala Phe Ser Thr Asn Val Val Ala Ser Lys Glu Leu  
 660 665 670  
 Gln Gln Pro Gly Ser Ala Arg Ser Thr Arg His Leu Glu Ile Glu Leu  
 675 680 685  
 25 Pro Lys Glu Ala Ser Tyr Gln Glu Gly Asp His Leu Gly Val Ile Pro  
 690 695 700  
 Arg Asn Tyr Glu Gly Ile Val Asn Arg Val Thr Ala Arg Phe Gly Leu  
 705 710 715 720  
 30 Asp Ala Ser Gln Gln Ile Arg Leu Glu Ala Glu Glu Glu Lys Leu Ala  
 725 730 735  
 His Leu Pro Leu Ala Lys Thr Val Ser Val Glu Glu Leu Leu Gln Tyr  
 35 740 745 750  
 Val Glu Leu Gln Asp Pro Val Thr Arg Thr Gln Leu Arg Ala Met Ala  
 755 760 765  
 Ala Lys Thr Val Cys Pro Pro His Lys Val Glu Leu Glu Ala Leu Leu  
 40 770 775 780  
 Glu Lys Gln Ala Tyr Lys Glu Gln Val Leu Ala Lys Arg Leu Thr Met  
 785 790 795 800  
 45 Leu Glu Leu Leu Glu Lys Tyr Pro Ala Cys Glu Met Lys Phe Ser Glu  
 805 810 815  
 Phe Ile Ala Leu Leu Pro Ser Ile Arg Pro Arg Tyr Tyr Ser Ile Ser

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72

820

825

830

Ser Ser Pro Arg Val Asp Glu Lys Gln Ala Ser Ile Thr Val Ser Val  
 835 840 845

5 Val Ser Gly Glu Ala Trp Ser Gly Tyr Gly Glu Tyr Lys Gly Ile Ala  
 850 855 860

Ser Asn Tyr Leu Ala Glu Leu Gln Glu Gly Asp Thr Ile Thr Cys Phe  
 865 870 875 880

10 Ile Ser Thr Pro Gln Ser Glu Phe Thr Leu Pro Lys Asp Pro Glu Thr  
 885 890 895

Pro Leu Ile Met Val Gly Pro Gly Thr Gly Val Ala Pro Phe Arg Gly  
 900 905 910

Phe Val Gln Ala Arg Lys Gln Leu Lys Glu Gln Gly Gln Ser Leu Gly  
 915 920 925

20 Glu Ala His Leu Tyr Phe Gly Cys Arg Ser Pro His Glu Asp Tyr Leu  
 930 935 940

Tyr Gln Glu Glu Leu Glu Asn Ala Gln Ser Glu Gly Ile Ile Thr Leu  
 945 950 955 960

25 His Thr Ala Phe Ser Arg Met Pro Asn Gln Pro Lys Thr Tyr Val Gln  
 965 970 975

His Val Met Glu Gln Asp Gly Lys Lys Leu Ile Glu Leu Leu Asp Gln  
 980 985 990

30 Gly Ala His Phe Tyr Ile Cys Gly Asp Gly Ser Gln Met Ala Pro Ala  
 995 1000 1005

Val Glu Ala Thr Leu Met Lys Ser Tyr Ala Asp Val His Gln Val Ser  
 1010 1015 1020

35 Glu Ala Asp Ala Arg Leu Trp Leu Gln Gln Leu Glu Glu Lys Gly Arg  
 1025 1030 1035 1040

Tyr Ala Lys Asp Val Trp Ala Gly  
 1045

40

45

20250101 142700